

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 17:27:49 ; Search time 69 Seconds
(without alignments)
2233.417 Million cell updates/sec

Title: US-10-750-623-21645
Perfect score: 599.6
Sequence: 1 tgggggtgagggaggcaaaca.....atacgacctgctctgtgtac 600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1669160 seqs, 128126992 residues

Total number of hits satisfying chosen parameters: 3338320

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US10_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS2/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		ID	Description
	No.	Score	Match	Length	DB			
c	1	35.4	5.9	4037	7	US-11-691-348-343	Sequence 343, App	
	2	33	5.5	982	7	US-11-514-704-15217	Sequence 15217, A	
c	3	33	5.5	2171	7	US-11-691-348-266	Sequence 266, App	
c	4	33	5.5	2176	7	US-11-691-348-3	Sequence 3, Appli	
	5	33	5.5	2581	7	US-11-514-704-15218	Sequence 15218, A	
c	6	33	5.5	3855	7	US-11-691-348-4	Sequence 4, Appli	
c	7	33	5.5	4015	7	US-11-691-348-1	Sequence 1, Appli	
c	8	33	5.5	4029	7	US-11-691-348-292	Sequence 292, App	
c	9	31.8	5.3	2394	7	US-11-514-704-7242	Sequence 7242, Ap	

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 17:27:49 ; Search time 142 Seconds
(without alignments)
2233.417 Million cell updates/sec

Title: US-10-750-623-61201
Perfect score: 1239
Sequence: 1 ccgactctttgcgacccctg.....tcttataatcccttgatatt 1239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1669160 seqs, 128126992 residues

Total number of hits satisfying chosen parameters: 3338320

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US10_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS2/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS2/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query						Description
	No.	Score	Match	Length	DB	ID	
c	1	153.2	12.4	15418	7	US-11-710-864-1	Sequence 1, Appli
	2	124.6	10.1	2573	1	US-10-533-069-2374	Sequence 2374, Ap
	3	102.4	8.3	85389	7	US-11-498-489-25	Sequence 25, Appl
	4	86.4	7.0	125958	7	US-11-505-577-26	Sequence 26, Appl
	5	58.8	4.7	42450	7	US-11-730-664-3	Sequence 3, Appli
c	6	40.6	3.3	2181	1	US-10-533-069-1945	Sequence 1945, Ap
	7	39	3.1	1003	1	US-10-438-246-27872	Sequence 27872, A
c	8	37.8	3.1	2596	7	US-11-514-704-12130	Sequence 12130, A
	9	37.4	3.0	2522	7	US-11-514-704-24510	Sequence 24510, A

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 17:10:22 ; Search time 3606 Seconds
(without alignments)
8154.244 Million cell updates/sec

Title: US-10-750-623-61201
Perfect score: 1239
Sequence: 1 ccgactctttgcgaccctg.....tcttataatcccttgatatt 1239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 31364175 seqs, 11865555624 residues

Total number of hits satisfying chosen parameters: 62728350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09D_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10J_PUBCOMB.seq:*
17: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10K_PUBCOMB.seq:*
18: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
19: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11B_PUBCOMB.seq:*
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24: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11G_PUBCOMB.seq:*
25: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11H_PUBCOMB.seq:*
26: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11I_PUBCOMB.seq:*
27: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11J_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				DB	ID	Description
	No.	Score	Query	Match	Length				
	1	1239	100.0	1239	11	US-10-750-185-61201			Sequence 61201, A
	2	1239	100.0	1239	11	US-10-750-623-61201			Sequence 61201, A
	3	1239	100.0	1239	15	US-10-750-622-61201			Sequence 61201, A
	4	599.6	48.4	600	11	US-10-750-185-21645			Sequence 21645, A
	5	599.6	48.4	600	11	US-10-750-623-21645			Sequence 21645, A
	6	599.6	48.4	600	15	US-10-750-622-21645			Sequence 21645, A
	7	215.4	17.4	1495	11	US-10-750-185-24940			Sequence 24940, A
	8	215.4	17.4	1495	11	US-10-750-623-24940			Sequence 24940, A
	9	215.4	17.4	1495	15	US-10-750-622-24940			Sequence 24940, A
	10	206.4	16.7	2407	11	US-10-750-185-33843			Sequence 33843, A
	11	206.4	16.7	2407	11	US-10-750-623-33843			Sequence 33843, A
	12	206.4	16.7	2407	15	US-10-750-622-33843			Sequence 33843, A
c	13	201.4	16.3	2548	11	US-10-750-185-27292			Sequence 27292, A
c	14	201.4	16.3	2548	11	US-10-750-623-27292			Sequence 27292, A
c	15	201.4	16.3	2548	15	US-10-750-622-27292			Sequence 27292, A
	16	201	16.2	31296	16	US-10-276-817B-3428			Sequence 3428, Ap
	17	201	16.2	32042	3	US-09-728-721-63			Sequence 63, Appl
	18	201	16.2	32042	7	US-10-118-984-44			Sequence 44, Appl
	19	201	16.2	32042	8	US-10-295-981-63			Sequence 63, Appl
	20	201	16.2	32042	11	US-10-843-188-63			Sequence 63, Appl
	21	201	16.2	34001	8	US-10-006-883A-15			Sequence 15, Appl
	22	201	16.2	39553	23	US-11-033-545-810			Sequence 810, App
	23	201	16.2	58111	23	US-11-033-545-673			Sequence 673, App
c	24	201	16.2	68571	8	US-10-401-194-1			Sequence 1, Appli
	25	197.2	15.9	305312	11	US-10-995-561-13236			Sequence 13236, A
c	26	193.4	15.6	157090	9	US-10-672-764A-34			Sequence 34, Appl
c	27	193.4	15.6	495635	11	US-10-737-082-12			Sequence 12, Appl
c	28	193.4	15.6	495635	11	US-10-765-790-12			Sequence 12, Appl
c	29	193.4	15.6	705636	11	US-10-737-082-30			Sequence 30, Appl
c	30	193.4	15.6	705636	11	US-10-765-790-30			Sequence 30, Appl
c	31	193.4	15.6	1237661	21	US-11-266-748A-29041			Sequence 29041, A
	32	192.4	15.5	2860	11	US-10-481-160-1			Sequence 1, Appli
c	33	191.6	15.5	3285	3	US-09-854-867-425			Sequence 425, App
c	34	191.6	15.5	3285	11	US-10-786-970A-425			Sequence 425, App
	35	190.8	15.4	413	3	US-09-960-352-10758			Sequence 10758, A
c	36	188.2	15.2	1000	21	US-11-266-748A-197063			Sequence 197063,
	37	188	15.2	466	4	US-09-925-065A-319604			Sequence 319604,
	38	188	15.2	466	5	US-09-925-065A-319604			Sequence 319604,
	39	188	15.2	466	13	US-10-301-480-394352			Sequence 394352,
	40	188	15.2	466	13	US-10-301-480-1007761			Sequence 1007761,
	41	188	15.2	558	4	US-09-925-065A-659902			Sequence 659902,
	42	188	15.2	558	5	US-09-925-065A-659902			Sequence 659902,
	43	186.8	15.1	558	4	US-09-925-065A-659901			Sequence 659901,
	44	186.8	15.1	558	5	US-09-925-065A-659901			Sequence 659901,
	45	185.2	14.9	102115	16	US-10-990-328-97355			Sequence 97355, A

rnpsm-21645

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 17:10:22 ; Search time 1746 Seconds
(without alignments)
8154.244 Million cell updates/sec

Title: US-10-750-623-21645
Perfect score: 599.6
Sequence: 1 tgggggtgagggaggcaaac.....atacgacctgctctgtgtac 600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 31364175 seqs, 11865555624 residues

Total number of hits satisfying chosen parameters: 62728350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09D_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10J_PUBCOMB.seq:*
17: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10K_PUBCOMB.seq:*
18: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
19: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11B_PUBCOMB.seq:*
20: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11C_PUBCOMB.seq:*
21: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11D_PUBCOMB.seq:*
22: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11E_PUBCOMB.seq:*
23: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11F_PUBCOMB.seq:*
24: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11G_PUBCOMB.seq:*
25: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11H_PUBCOMB.seq:*
26: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11I_PUBCOMB.seq:*
27: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11J_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	599.6	100.0	600	11	US-10-750-185-21645	Sequence 21645, A
2	599.6	100.0	600	11	US-10-750-623-21645	Sequence 21645, A
3	599.6	100.0	600	15	US-10-750-622-21645	Sequence 21645, A
4	599.6	100.0	1239	11	US-10-750-185-61201	Sequence 61201, A
5	599.6	100.0	1239	11	US-10-750-623-61201	Sequence 61201, A
6	599.6	100.0	1239	15	US-10-750-622-61201	Sequence 61201, A
7	202.2	33.7	31296	16	US-10-276-817B-3428	Sequence 3428, Ap
8	202.2	33.7	32042	3	US-09-728-721-63	Sequence 63, Appl
9	202.2	33.7	32042	7	US-10-118-984-44	Sequence 44, Appl
10	202.2	33.7	32042	8	US-10-295-981-63	Sequence 63, Appl
11	202.2	33.7	32042	11	US-10-843-188-63	Sequence 63, Appl
12	202.2	33.7	34001	8	US-10-006-883A-15	Sequence 15, Appl
13	202.2	33.7	39553	23	US-11-033-545-810	Sequence 810, App
14	202.2	33.7	58111	23	US-11-033-545-673	Sequence 673, App
c 15	202.2	33.7	68571	8	US-10-401-194-1	Sequence 1, Appli
16	72	12.0	3080	3	US-09-728-721-25	Sequence 25, Appl
17	72	12.0	3080	7	US-10-105-931-25	Sequence 25, Appl
18	72	12.0	3080	7	US-10-118-984-25	Sequence 25, Appl
19	72	12.0	3080	8	US-10-006-883A-94	Sequence 94, Appl
20	72	12.0	3080	8	US-10-295-981-25	Sequence 25, Appl
21	72	12.0	3080	11	US-10-843-188-25	Sequence 25, Appl
22	72	12.0	4608	11	US-10-956-157-4599	Sequence 4599, Ap
23	72	12.0	4610	8	US-10-006-883A-11	Sequence 11, Appl
24	72	12.0	4610	16	US-10-917-503-18312	Sequence 18312, A
25	72	12.0	4613	26	US-11-443-428A-443967	Sequence 443967,
26	69.4	11.6	536	3	US-09-764-855-30.	Sequence 30, Appl
27	69.4	11.6	536	7	US-10-072-349-30	Sequence 30, Appl
28	69.4	11.6	2224	26	US-11-443-428A-443971	Sequence 443971,
29	69.4	11.6	2614	26	US-11-443-428A-443977	Sequence 443977,
30	69.4	11.6	2859	3	US-09-728-721-9	Sequence 9, Appli
31	69.4	11.6	2859	7	US-10-105-931-9	Sequence 9, Appli
32	69.4	11.6	2859	7	US-10-118-984-9	Sequence 9, Appli
33	69.4	11.6	2859	8	US-10-295-981-9	Sequence 9, Appli
34	69.4	11.6	2859	11	US-10-843-188-9	Sequence 9, Appli
35	69.4	11.6	2859	11	US-10-966-846-3	Sequence 3, Appli
36	69.4	11.6	3382	3	US-09-728-721-7	Sequence 7, Appli
37	69.4	11.6	3382	7	US-10-105-931-7	Sequence 7, Appli
38	69.4	11.6	3382	7	US-10-118-984-7	Sequence 7, Appli
39	69.4	11.6	3382	8	US-10-295-981-7	Sequence 7, Appli
40	69.4	11.6	3382	11	US-10-843-188-7	Sequence 7, Appli
41	69.4	11.6	3382	11	US-10-966-846-1	Sequence 1, Appli
42	69.4	11.6	3589	26	US-11-443-428A-443975	Sequence 443975,
43	69.4	11.6	3616	26	US-11-443-428A-443972	Sequence 443972,
44	69.4	11.6	3789	7	US-10-013-477-10	Sequence 10, Appl
45	69.4	11.6	3789	16	US-10-100-683-4255	Sequence 4255, Ap

mi-21645

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:58:39 ; Search time 351 Seconds
(without alignments)
6408.357 Million cell updates/sec

Title: US-10-750-623-21645
Perfect score: 599.6
Sequence: 1 tgggggtgagggaggcaaaca.....atacgacctgctctgtgtac 600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: 10310350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS2/ptodata/1/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS2/ptodata/1/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS2/ptodata/1/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS2/ptodata/1/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS2/ptodata/1/ina/7A_COMB.seq:*
6: /EMC_Celerra_SIDS2/ptodata/1/ina/7B_COMB.seq:*
7: /EMC_Celerra_SIDS2/ptodata/1/ina/H_COMB.seq:*
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11: /EMC_Celerra_SIDS2/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	202.2	33.7	32042	3	US-09-245-281-44	Sequence 44, Appl
2	202.2	33.7	32042	3	US-09-340-620A-63	Sequence 63, Appl
3	202.2	33.7	32042	3	US-09-728-721-63	Sequence 63, Appl
4	202.2	33.7	32042	5	US-10-118-984-44	Sequence 44, Appl
5	202.2	33.7	39553	3	US-09-949-002-810	Sequence 810, App
6	202.2	33.7	58111	3	US-09-949-002-673	Sequence 673, App

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:58:39 ; Search time 724 Seconds
 (without alignments)
 6408.357 Million cell updates/sec

Title: US-10-750-623-61201
 Perfect score: 1239
 Sequence: 1 ccgactctttgcgacccctg.....tcttataatcccttgatattt 1239

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: 10310350

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*
 1: /EMC_Celerra_SIDS2/ptodata/1/ina/1_COMB.seq:*
 2: /EMC_Celerra_SIDS2/ptodata/1/ina/5_COMB.seq:*
 3: /EMC_Celerra_SIDS2/ptodata/1/ina/6A_COMB.seq:*
 4: /EMC_Celerra_SIDS2/ptodata/1/ina/6B_COMB.seq:*
 5: /EMC_Celerra_SIDS2/ptodata/1/ina/7A_COMB.seq:*
 6: /EMC_Celerra_SIDS2/ptodata/1/ina/7B_COMB.seq:*
 7: /EMC_Celerra_SIDS2/ptodata/1/ina/H_COMB.seq:*
 8: /EMC_Celerra_SIDS2/ptodata/1/ina/PCTUS_COMB.seq:*
 9: /EMC_Celerra_SIDS2/ptodata/1/ina/PP_COMB.seq:*
 10: /EMC_Celerra_SIDS2/ptodata/1/ina/RE_COMB.seq:*
 11: /EMC_Celerra_SIDS2/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query			ID	Description
		Match	Length	DB		
1	201	16.2	32042	3	US-09-245-281-44	Sequence 44, Appl
2	201	16.2	32042	3	US-09-340-620A-63	Sequence 63, Appl
3	201	16.2	32042	3	US-09-728-721-63	Sequence 63, Appl
4	201	16.2	32042	5	US-10-118-984-44	Sequence 44, Appl
5	201	16.2	39553	3	US-09-949-002-810	Sequence 810, App
6	201	16.2	58111	3	US-09-949-002-673	Sequence 673, App

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:45:26 ; Search time 4064 Seconds
(without alignments)
18914.697 Million cell updates/sec

Title: US-10-750-623-61201
Perfect score: 1239
Sequence: 1 ccgactctttgcgacccctg.....tcttataatcccttgatatt 1239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_est13:*
12: gb_est12:*
13: gb_est11:*
14: gb_est10:*
15: gb_gss1:*
16: gb_gss2:*
17: gb_gss3:*
18: gb_gss4:*
19: gb_gss5:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query

No.	Score	Match	Length	DB	ID	Description			
c	1	249	20.1	605	19	CT185030	CT185030	Sus	scrof
	2	249	20.1	864	19	CT265370	CT265370	Sus	scrof
c	3	247.6	20.0	814	19	CT438819	CT438819	Sus	scrof
c	4	246	19.9	779	19	CT372765	CT372765	Sus	scrof
	5	246	19.9	885	19	CT425116	CT425116	Sus	scrof
c	6	244.4	19.7	829	19	CT102470	CT102470	Sus	scrof
	7	242.6	19.6	808	19	CT445831	CT445831	Sus	scrof
c	8	241.4	19.5	722	19	CT267357	CT267357	Sus	scrof
	9	241.4	19.5	752	17	CL373561	CL373561	RPCI44_45	
c	10	241.4	19.5	811	19	CT440825	CT440825	Sus	scrof
	11	239.6	19.3	871	19	CT473538	CT473538	Sus	scrof
c	12	239.6	19.3	872	19	CT316901	CT316901	Sus	scrof
	13	239.6	19.3	915	19	CT224928	CT224928	Sus	scrof
c	14	239	19.3	917	19	CT379372	CT379372	Sus	scrof
	15	238.8	19.3	831	19	CT380271	CT380271	Sus	scrof
c	16	238.6	19.3	841	19	CT465534	CT465534	Sus	scrof
	17	238	19.2	714	19	CT100278	CT100278	Sus	scrof
c	18	238	19.2	801	19	CT475998	CT475998	Sus	scrof
	19	238	19.2	806	19	CT320919	CT320919	Sus	scrof
c	20	238	19.2	809	19	CT248002	CT248002	Sus	scrof
	21	238	19.2	812	19	CT396728	CT396728	Sus	scrof
c	22	238	19.2	824	19	CT442943	CT442943	Sus	scrof
	23	238	19.2	837	19	CT200491	CT200491	Sus	scrof
c	24	238	19.2	839	19	CT264675	CT264675	Sus	scrof
	25	238	19.2	882	19	CT467508	CT467508	Sus	scrof
c	26	238	19.2	884	19	CT373719	CT373719	Sus	scrof
	27	236.4	19.1	741	19	CT335577	CT335577	Sus	scrof
c	28	236.4	19.1	760	19	CT452143	CT452143	Sus	scrof
	29	236.4	19.1	792	19	CT269294	CT269294	Sus	scrof
c	30	236.4	19.1	804	19	CT285571	CT285571	Sus	scrof
	31	236.4	19.1	809	19	CT313761	CT313761	Sus	scrof
c	32	236.4	19.1	829	19	CT293886	CT293886	Sus	scrof
	33	236.4	19.1	830	19	CT130537	CT130537	Sus	scrof
c	34	236.4	19.1	860	19	CT350038	CT350038	Sus	scrof
	35	236.4	19.1	873	19	CT244745	CT244745	Sus	scrof
c	36	236.4	19.1	882	19	CT329087	CT329087	Sus	scrof
	37	236.4	19.1	891	19	CT447279	CT447279	Sus	scrof
c	38	236.4	19.1	900	19	CT130475	CT130475	Sus	scrof
	39	235.8	19.0	894	19	CT399477	CT399477	Sus	scrof
c	40	235	19.0	793	19	CT369120	CT369120	Sus	scrof
	41	234.8	19.0	695	17	CL323492	CL323492	RPCI44_45	
c	42	234.8	19.0	745	17	CL382186	CL382186	RPCI44_32	
	43	234.8	19.0	781	19	CT293222	CT293222	Sus	scrof
c	44	234.8	19.0	782	19	CT410916	CT410916	Sus	scrof
	45	234.8	19.0	785	19	CT326765	CT326765	Sus	scrof

ALIGNMENTS

RESULT 1

CT185030

LOCUS CT185030 605 bp DNA linear GSS 02-NOV-2005

DEFINITION Sus scrofa genomic clone CH242-113I11, genomic survey sequence.

ACCESSION CT185030

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:45:26 ; Search time 1968 Seconds
(without alignments)
18914.697 Million cell updates/sec

Title: US-10-750-623-21645

Perfect score: 599.6

Sequence: 1 tggggtgagggaggcaaaca.....atacgacctgctctgtgtac 600

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_hlc:*

7: gb_est2:*

8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_est13:*
 12: gb_est12:*
 13: gb_est11:*
 14: gb_est10:*
 15: gb_gss1:*
 16: gb_gss2:*
 17: gb_gss3:*
 18: gb_gss4:*
 19: gb_gss5:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

		%						
Result	Query							
No.	Score	Match	Length	DB	ID	Description		

1	188.6	31.5	3124	6	BC020114	BC020114 Homo sapi		
2	154.2	25.7	644	17	CL371847	CL371847 RPCI44_30		
3	85.8	14.3	823	10	CO886987	CO886987 BovGen_15		
4	85.8	14.3	1133	12	DV793189	DV793189 Hw_loin_E		
5	75	12.5	542	2	BE633255	BE633255 uv74g04.y		
6	72	12.0	891	8	CF618769	CF618769 AGENCOURT		
7	72	12.0	907	8	CF618768	CF618768 AGENCOURT		
8	69.4	11.6	2862	19	AY418482	AY418482 Homo sapi		
9	68.4	11.4	697	4	BP151920	BP151920 BP151920		
c 10	66.4	11.1	509	4	BQ327671	BQ327671 MR1-RT003		
11	66	11.0	1134	3	BM549076	BM549076 AGENCOURT		
12	61	10.2	849	12	DV814288	DV814288 LB01712.C		
13	58.8	9.8	773	1	AI561834	AI561834 vk33g03.y		
14	58.6	9.8	932	4	BQ900609	BQ900609 AGENCOURT		
15	58.2	9.7	433	1	AI607231	AI607231 vo63c02.y		

ge-61201

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:45:12 ; Search time 8383 Seconds
(without alignments)
10216.382 Million cell updates/sec

Title: US-10-750-623-61201
Perfect score: 1239
Sequence: 1 ccgactctttgcgacccctg.....tcttataatcccttgatatt 1239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB	Query		
c	1	1190.8	96.1	332533	12	AC152664	AC152664	Bos tauru
	2	1186	95.7	188320	12	AC092085	AC092085	Bos tauru

rgl-21645

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:45:12 ; Search time 4059 Seconds
(without alignments)
10216.382 Million cell updates/sec

Title: US-10-750-623-21645
Perfect score: 599.6
Sequence: 1 tgggggtgagggaggcaaaca.....atacgacctgctctgtgtac 600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	% Length	DB ID	Description
c	1	587.6	98.0	188320	12 AC092085	AC092085 Bos tauru
c	2	587.6	98.0	211084	12 AC092084	AC092084 Bos tauru

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:43:54 ; Search time 999 Seconds
(without alignments)
9189.503 Million cell updates/sec

Title: US-10-750-623-61201
Perfect score: 1239
Sequence: 1 ccgactcttttgcgacccctg.....tcttataatcccttgtattt 1239

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	201	16.2	32042	2	AAZ09252	Aaz09252 Human CAR

rng-21645

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OM nucleic - nucleic search, using sw model

Run on: September 12, 2007, 16:43:54 ; Search time 484 Seconds
(without alignments)
9189.503 Million cell updates/sec

Title: US-10-750-623-21645
Perfect score: 599.6
Sequence: 1 tgggggtgagggaggcaaca.....atacgacctgctctgtgtac 600

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					Description
No.	Score	Match	Length	DB	ID		
1	202.2	33.7	32042	2	AAZ09252		Aaz09252 Human CAR